

Application No. 08/477,316  
Attorney's Docket No. 028723-060

1  
F wherein the chromosomal material is present in a morphologically identifiable cell nucleus;  
allowing said probe to bind to said targeted chromosomal material; and detecting said bound  
probe, wherein bound probe is indicative of the presence of target chromosomal material.

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2  
F 2 48. (Three Times Amended) A method of staining targeted interphase chromosomal  
material based upon a nucleic acid segment employing a unique sequence high complexity  
nucleic acid probe of greater than about 40 kb, wherein said targeted chromosomal material is  
a genetic rearrangement associated with at least one chromosome in humans, said method  
comprising contacting said chromosomal material with a unique sequence high complexity  
nucleic acid probe of greater than about 40 kb, wherein the chromosomal material is present in  
a morphologically identifiable cell nucleus; allowing said probe to bind to said targeted  
chromosomal material; and detecting said bound probe, wherein bound probe is indicative of  
the presence of target chromosomal material.

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3  
F 3 50. (Three Times Amended) A method of staining targeted interphase chromosomal  
material based upon a nucleic acid segment employing a unique sequence high complexity  
nucleic acid probe of greater than about 50,000 bases, wherein said targeted interphase  
chromosomal material is a genetic rearrangement associated with at least one chromosome in  
humans, said method comprising contacting said interphase chromosomal material with a  
unique sequence high complexity nucleic acid probe of greater than about 50,000 bases,  
wherein the chromosomal material is present in a morphologically identifiable cell nucleus;  
allowing said probe to bind to said targeted interphase chromosomal material; and detecting  
said bound probe, wherein bound probe is indicative of the presence of target interphase  
chromosomal material.

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[ Please add the following new claims:

-- 12 59. The method of claim 48<sup>2</sup>, wherein complexity of the unique sequence high complexity nucleic acid probe is greater than about 100,000 bases.

F<sup>4</sup> 13 60. The method of claim 50<sup>3</sup>, wherein complexity of the unique sequence high complexity nucleic acid probe is greater than about 100,000 bases. - -